

SEQ ID NO: 1
LENGTH: 524
TYPE: amino acid
TOPOLOGY: linear
KIND: peptide
SEQUENCE

43

44

SEQ ID NO: 2
 LENGTH: 1575
 TYPE: nucleic acid
 NUMBER OF CHAIN: single strand
 TOPOLOGY: linear
 KIND: cDNA to mRNA
 SEQUENCE

ATG AAT CTG CAT GTG GTG AAA TGG AAA TTA TCT GTT GTC AGT GTG CTG	48
Met Asn Leu His Val Val Lys Trp Lys Leu Ser Val Val Ser Val Leu	
5 10 15	
ATC ACA TTG TAC TAC AGT CAC ACT GTT GCT CTC AGC CTG AAG GAA CAT	96
Ile Thr Leu Tyr Tyr Ser His Thr Val Ala Leu Ser Leu Lys Glu His	
20 25 30	
CTG GCT GAT TGT CTT GAA GAC AAA GAC TAT GAC ACG CTG CTG CAG ACT	144
Leu Ala Asp Cys Leu Glu Asp Lys Asp Tyr Asp Thr Leu Leu Gln Thr	
35 40 45	
CTG GAT AAC GGT CTT OCA CAC ATT AAC ACG TCT CAT CAT GTG GTT ATA	192
Leu Asp Asn Gly Leu Pro His Ile Asn Thr Ser His His Val Val Ile	
50 55 60	
GTC GGA GCT GGC ATG GOC GGA CTG ACG GCG GOC AAG TTA CTG CAA GAC	240
Val Gly Ala Gly Met Ala Gly Leu Thr Ala Ala Lys Leu Leu Gln Asp	
65 70 75 80	
GCA GGA CAC ACG GTA ACC ATA TTG GAG GCT AAT GAT CGT GTT GGA GGA	288
Ala Gly His Thr Val Thr Ile Leu Glu Ala Asn Asp Arg Val Gly Gly	
81 85 90 95	
CGT GTG GAG AOC TAC AGG AAT GAA AAA GAA GGC TGG TAT GCT GAA ATG	336
Arg Val Glu Thr Tyr Arg Asn Glu Lys Glu Gly Trp Tyr Ala Glu Met	
100 105 110	
GGA GCT ATG AGG ATC OCA AGC TCT CAC GGC ATC GTC CAG TGG TTT GTC	384
Gly Ala Met Arg Ile Pro Ser Ser His Arg Ile Val Gln Trp Phe Val	
115 120 125	
AAA AAG CTT GGG GTC GAG ATG AAT GAG TTC GTC ATG ACT GAT GAC AAC	432
Lys Lys Leu Gly Val Glu Met Asn Glu Phe Val Met Thr Asp Asp Asn	
130 135 140	
AOC TTT TAC CTG GTT AAT GGG GTG CGG GAG AGG ACA TAT GTT GTT CAA	480
Thr Phe Tyr Leu Val Asn Gly Val Arg Glu Arg Thr Tyr Val Val Gln	
145 150 155 160	
GAA AAC OCT GAT GTC CTG AAG TAC AAC GTG TCA GAA AGC GAG AAG GGA	528
Glu Asn Pro Asp Val Leu Lys Tyr Asn Val Ser Glu Ser Glu Lys Gly	
165 170 175	

ATT TCA GGC GAT GAT CTG CTA GAT CGA GCT TTG CAG AAG GTG AAA GAG	576
Ile Ser Ala Asp Asp Leu Leu Asp Arg Ala Leu Gln Lys Val Lys Glu	
180 185 190	
GAA GTG GAA GCA AAT GGT TGT AAA GCT GCA CTG GAA AAA TAC GAC CGC	624
Glu Val Glu Ala Asn Gly Cys Lys Ala Ala Leu Glu Lys Tyr Asp Arg	
195 200 205	
TAT TCT GTG AAG GAG TAT CTG AAA GAA GAA GGT GGT TTG AGT OCA GGA	672
Tyr Ser Val Lys Glu Tyr Leu Lys Glu Glu Gly Gly Leu Ser Pro Gly	
210 215 220	
GCA GTG AGG ATG ATT GGA GAC CTG CTG AAT GAA CAG AGC CTC ATG TAC	720
Ala Val Arg Met Ile Gly Asp Leu Leu Asn Glu Gln Ser Leu Met Tyr	
225 230 235 240	
ACA GCG CTG AGT GAG ATG ATC TAC GAC CAG GCT GAC GTC AAT GAC AGT	768
Thr Ala Leu Ser Glu Met Ile Tyr Asp Gln Ala Asp Val Asn Asp Ser	
245 250 255	
GTC ACG TAT CAT GAA GTG ACG GGT GGA TCA GAT CTT CTT CCC GAA GCT	816
Val Thr Tyr His Glu Val Thr Gly Gly Ser Asp Leu Leu Pro Glu Ala	
260 265 270	
TTT CTT TCT GTC CTG GAT GTC CCC ATC CTC TTA AAC TOC AAA GTC AAA	864
Phe Leu Ser Val Leu Asp Val Pro Ile Leu Leu Asn Ser Lys Val Lys	
275 280 285	
CAC ATC AGG CAG TCA GAT AAA GGT GTA ATC GTG TCA TAC CAG ACA GGC	912
His Ile Arg Gln Ser Asp Lys Gly Val Ile Val Ser Tyr Gln Thr Gly	
290 295 300	
AAT GAG TOC TCT TTG ATG GAC CTT TCT GCT GAC ATT GTT CTG GTA ACA	960
Asn Glu Ser Ser Leu Met Asp Leu Ser Ala Asp Ile Val Leu Val Thr	
305 310 315 320	
ACC ACA GGC AAA GCA GGC CTC TTC ATA GAC TTT GAT CCA OCT CTC TOC	1008
Thr Thr Ala Lys Ala Ala Leu Phe Ile Asp Phe Asp Pro Pro Leu Ser	
325 330 335	
ATC AGT AAG ATG GAG GGC CTC CGG TCA GTC CAC TAT GAC AGC TOC ACT	1056
Ile Ser Lys Met Glu Ala Leu Arg Ser Val His Tyr Asp Ser Ser Thr	
340 345 350	
AAA ATC CTC CTC ACC TTT CGC GAT AAG TTC TGG GAG GAC GAT GGC ATC	1104
Lys Ile Leu Leu Thr Phe Arg Asp Lys Phe Trp Glu Asp Asp Gly Ile	
355 360 365	
CGA GGA GGC AAG AGC ATT ACC GAT GGA OCT TCT CGT TAC ATC TAC TAT	1152
Arg Gly Gly Lys Ser Ile Thr Asp Gly Pro Ser Arg Tyr Ile Tyr Tyr	
370 375 380	
CCC AGC CAC AGT TTC CAT ACA AAT GAG ACC ATT GGA GTC CTC CTG GCA	1200
Pro Ser His Ser Phe His Thr Asn Glu Thr Ile Gly Val Leu Leu Ala	
385 390 395 400	

TOC TAC ACT TGG TCT GAC GAG TOC CTC CTC TTC CTG GGT GCA AGC GAT	1248
Ser Tyr Thr Trp Ser Asp Glu Ser Leu Leu Phe Leu Gly Ala Ser Asp	
405 410 415	
GAA GAG CTG AAA GAG CTG GOC CTG AGA GAT CTG GCA AAA ATC CAC GGT	1296
Glu Glu Leu Lys Glu Leu Ala Leu Arg Asp Leu Ala Lys Ile His Gly	
420 425 430	
GAG CAA GTC TGG GAT AAG TOC ACG GGA GTC ATA GTG AAG AAG TGG AGC	1344
Glu Gln Val Trp Asp Lys Cys Thr Gly Val Ile Val Lys Lys Trp Ser	
435 440 445	
GCT GAT OCT TAC AGC TTG GGC GOC TTC GCT CTC TTC ACA CCC TAC CAA	1392
Ala Asp Pro Tyr Ser Leu Gly Ala Phe Ala Leu Phe Thr Pro Tyr Gln	
450 455 460	
CAC TTG GAG TAC GCT CAG GAG CTC TTC AGC AGC GAG GGC AGG GTG CAC	1440
His Leu Glu Tyr Ala Gln Glu Leu Phe Ser Ser Glu Gly Arg Val His	
465 470 475 480	
TTT GCT GGT GAA CAC ACA GOC TTC CCT CAT GCT TGG ATC GAA ACG TCT	1488
Phe Ala Gly Glu His Thr Ala Phe Pro His Ala Trp Ile Glu Thr Ser	
485 490 495	
ATG AAA TCT GCA ATC AGG GCT GCT ACA AAT ATT AAT AAA GTG GCA AAT	1536
Met Lys Ser Ala Ile Arg Ala Ala Thr Asn Ile Asn Lys Val Ala Asn	
500 505 510	
GAA GAG TCA ACT ATA GAA CAT ACA AAA GAT GAG CTG TAG	1575
Glu Glu Ser Thr Ile Glu His Thr Lys Asp Glu Leu	
515 520	